

SEQUENCE LISTING

<110> Xu, Wenfeng
Lofton-Day, Catherine E.
Henne, Randall
Presnell, Scott R.
Yao, Yue
Novak, Julia E.
Foster, Donald C.
Yee, David P.

<120> UMLR POLYPEPTIDES

<130> 99-75

<150> US 60/160,880

<151> 1999-10-22

<150> US 60/163,215

<151> 1999-11-02

<150> US 60/218,769

<151> 2000-07-17

<150> US 60/222,221

<151> 2000-08-01

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<211> 1162

<212> DNA

<213> Homo sapiens

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ttc ttc aac aga cat tgc cag cgt gga ggt ttg ctg cag ttt gag gct 643
 Phe Phe Asn Arg His Cys Gln Arg Gly Gly Leu Leu Gln Phe Glu Ala
 165 170 175 180

gat aaa aca gca aag gag gaa tct ctc ttc ccc gtg cca ccc agc aag 691
 Asp Lys Thr Ala Lys Glu Glu Ser Leu Phe Pro Val Pro Pro Ser Lys
 185 190 195

gag acc agt gct gag tcc caa gag tcc ttt acc atg gcc tcc tgc acc 739
 Glu Thr Ser Ala Glu Ser Gln Glu Ser Phe Thr Met Ala Ser Cys Thr
 200 205 210

tca gag agc cac tcc cac tgg gtc cac agc ccc atc gaa tgc aca gag 787
 Ser Glu Ser His Ser His Trp Val His Ser Pro Ile Glu Cys Thr Glu
 215 220 225

ctg gac ctg caa aag ttt tcc agc tct gcc tcc tat act gga gct gag 835
 Leu Asp Leu Gln Lys Phe Ser Ser Ser Ala Ser Tyr Thr Gly Ala Glu
 230 235 240

acc ttg ggg gga aac aca gtc gaa agc act gga gac agg ctg gag ctc 883
 Thr Leu Gly Gly Asn Thr Val Glu Ser Thr Gly Asp Arg Leu Glu Leu
 245 250 255 260

aat gtg ccc ttt gaa gtt ccc agc cct taa ctctaagag gtctcttggg 933
 Asn Val Pro Phe Glu Val Pro Ser Pro *
 265

cccctggcag ccttgcccag ttgttctctc tggactctgt tcctatacca caacagcagc 993
 aggggctga aatgtgatgt ccacaagagc taatacccta cagatggggc atatcctatc 1053
 ccatcccacc agaggattga ttctccattt cacaaggact gatctggagc atttcttgct 1113
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<210> 2

<211> 269

<212> PRT

<213> Homo sapiens

<400> 2

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 20 25 30
 Tyr Gly Glu Gly Gly Asp Ala Tyr Cys Thr Ala Cys Pro Pro Arg Arg
 35 40 45
 Tyr Lys Ser Ser Trp Gly His His Lys Cys Gln Ser Cys Ile Thr Cys
 50 55 60
 Ala Val Ile Asn Arg Val Gln Lys Val Asn Cys Thr Ala Thr Ser Asn
 65 70 75 80
 Ala Val Cys Gly Asp Cys Leu Pro Arg Phe Tyr Arg Lys Thr Arg Ile
 85 90 95
 Gly Gly Leu Gln Asp Gln Glu Cys Ile Pro Cys Thr Lys Gln Thr Pro
 100 105 110
 Thr Ser Glu Val Gln Cys Ala Phe Gln Leu Ser Leu Val Glu Ala Asp
 115 120 125
 Ala Pro Thr Val Pro Pro Gln Glu Ala Thr Leu Val Ala Leu Val Ser
 130 135 140
 Ser Leu Leu Val Val Phe Thr Leu Ala Phe Leu Gly Leu Phe Phe Leu
 145 150 155 160
 Tyr Cys Lys Gln Phe Phe Asn Arg His Cys Gln Arg Gly Gly Leu Leu
 165 170 175
 Gln Phe Glu Ala Asp Lys Thr Ala Lys Glu Glu Ser Leu Phe Pro Val
 180 185 190
 Pro Pro Ser Lys Glu Thr Ser Ala Glu Ser Gln Glu Ser Phe Thr Met
 195 200 205
 Ala Ser Cys Thr Ser Glu Ser His Ser His Trp Val His Ser Pro Ile
 210 215 220
 Glu Cys Thr Glu Leu Asp Leu Gln Lys Phe Ser Ser Ser Ala Ser Tyr
 225 230 235 240
 Thr Gly Ala Glu Thr Leu Gly Gly Asn Thr Val Glu Ser Thr Gly Asp
 245 250 255
 Arg Leu Glu Leu Asn Val Pro Phe Glu Val Pro Ser Pro
 260 265

<210> 3

<211> 807

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<213> Artificial Sequence

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<223> degenerate sequence

<221> misc_feature

<222> (1)...(807)

<223> n = A,T,C or G

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tgyacngcnt	gyccnccnmg	nmgntayaar	wsnwsntggg	gncaycayaa	rtgycarwsn	180
tgyathacnt	gygcngtnat	haaymgngtn	caraargtna	aytgyacngc	nacnwsnaay	240
gcngtntgyg	gngaytgyyt	nccnmgntty	taymgnaara	cnmgcnathgg	nggnytnear	300
gaycargart	gyathccttg	yacnaarcar	acnccnacnw	sngargtnca	rtgygcntty	360
carytnwsny	tngtngargc	ngaygcncn	acngtncnc	cncargargc	nacnytngt	420
gcnytngtnw	snwsnytnyt	ngtngntty	acnytnngnt	tyytnngny	nttyttytn	480
taytgyaarc	arttyttyaa	ymgncaytg	carmgngng	gnytnytnc	rttygargcn	540
gayaaracng	cnaargarga	rwsnytnntty	ccngtncnc	cnwsnaarga	racnwsngcn	600
garwsncarg	arwsnttyac	natggcnwsn	tgyacnwsng	arwsncayws	ncaytgggtn	660
caywsnccna	thgartgyac	ngarytngay	ytncaraart	tywsnwsnws	ngcnwsntay	720
acngngcng	aracnytnng	nggnaayacn	gtngarwsna	cngngaymg	nytngarytn	780
aaygtncnt	tygargtncc	nwsnccn				807

<210> 4

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<223> Pseudo repeat motif #1

<221> VARIANT

<222> (1)...(1)

<223> Xaa is any amino acid residue

<221> VARIANT

<222> (3)...(12)

<223> Each Xaa is independently any amino acid residue

<221> VARIANT

<222> (13)...(16)

<223> Each Xaa is independently any amino acid residue
or not present

<221> VARIANT

<222> (19)...(20)

<223> Each Xaa is independently any amino acid residue

<221> VARIANT
 <222> (22)...(26)
 <223> Each Xaa is independently any amino acid residue

<221> VARIANT
 <222> (27)...(30)
 <223> Each Xaa is independently any amino acid residue
 or not present

<221> VARIANT
 <222> (32)...(37)
 <223> Each Xaa is independently any amino acid residue
 or not present

<221> VARIANT
 <222> (38)...(39)
 <223> Each Xaa is independently any amino acid residue
 or not present

<221> VARIANT
 <222> (41)...(41)
 <223> Xaa is any amino acid residue

<400> 4
 Xaa Cys Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
 1 5 10 15
 Cys Cys Xaa Xaa Cys Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Cys Xaa
 20 25 30
 Xaa Xaa Xaa Xaa Xaa Xaa Xaa Cys Xaa
 35 40

<210> 5
 <211> 45
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Pseudo repeat motif #2

<221> VARIANT
 <222> (1)...(1)
 <223> Xaa is any amino acid residue

<221> VARIANT
 <222> (3)...(15)
 <223> Each Xaa is independently any amino acid residue

<221> VARIANT
 <222> (16)...(17)
 <223> Each Xaa is independently any amino acid residue
 or not present

<221> VARIANT
 <222> (19)...(20)
 <223> Each Xaa is independently any amino acid residue

<221> VARIANT
 <222> (22)...(23)
 <223> Each Xaa is independently any amino acid residue

<221> VARIANT
 <222> (24)...(24)
 <223> Each Xaa is independently any amino acid residue
 or not present

<221> VARIANT
 <222> (26)...(33)
 <223> Each Xaa is independently any amino acid residue

<221> VARIANT
 <222> (34)...(36)
 <223> Each Xaa is independently any amino acid residue
 or not present

<221> VARIANT
 <222> (38)...(44)
 <223> Each Xaa is independently any amino acid residue

<400> 5

Xaa	Cys	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa
1			5				10					15			
Xaa	Cys	Xaa	Xaa	Cys	Xaa	Xaa	Xaa	Cys	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa
			20				25					30			
Xaa	Xaa	Xaa	Xaa	Cys	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Cys		
			35				40						45		

<210> 6
<211> 49
<212> PRT
<213> Artificial Sequence

<220>
<223> Pseudo repeat motif #3

<221> VARIANT
<222> (1)...(1)
<223> Xaa is any amino acid residue

<221> VARIANT
<222> (3)...(7)
<223> Each Xaa is independently any amino acid residue

<221> VARIANT
<222> (8)...(8)
<223> Xaa is any amino acid residue or not present

<221> VARIANT
<222> (9)...(14)
<223> Each Xaa is independently any amino acid residue

<221> VARIANT
<222> (15)...(18)
<223> Each Xaa is independently any amino acid residue
or not present

<221> VARIANT
<222> (20)...(21)
<223> Each Xaa is independently any amino acid residue

<221> VARIANT
<222> (23)...(24)
<223> Each Xaa is independently any amino acid residue

<221> VARIANT
<222> (25)...(29)
<223> Each Xaa is independently any amino acid residue
or not present

<221> VARIANT

<222> (31)...(38)

<223> Each Xaa is independently any amino acid residue

<221> VARIANT

<222> (39)...(39)

<223> Xaa is any amino acid residue or not present

<221> VARIANT

<222> (41)...(47)

<223> Each Xaa is independently any amino acid residue

<221> VARIANT

<222> (49)...(49)

<223> Xaa is any amino acid residue or not present

<400> 6

Xaa	Cys	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa
1			5				10					15				
Xaa	Xaa	Cys	Xaa	Xaa	Cys	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Cys	Xaa	Xaa	
			20				25					30				
Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Cys	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Cys	
			35				40					45				
Xaa																

<210> 7

<211> 48

<212> PRT

<213> Artificial Sequence

<220>

<223> Pseudo repeat motif #3 alternative motif

<221> VARIANT

<222> (1)...(1)

<223> Xaa is any amino acid residue

<221> VARIANT

<222> (3)...(7)

<223> Each Xaa is independently any amino acid residue

<221> VARIANT

<222> (8)...(8)

<223> Xaa is independently any amino acid residue or not present

<221> VARIANT

<222> (10)...(13)

<223> Each Xaa is independently any amino acid residue

<221> VARIANT

<222> (14)...(18)

<223> Each Xaa is independently any amino acid residue or not present

<221> VARIANT

<222> (20)...(21)

<223> Each Xaa is independently any amino acid residue

<221> VARIANT

<222> (23)...(24)

<223> Each Xaa is independently any amino acid residue

<221> VARIANT

<222> (25)...(29)

<223> Each Xaa is independently any amino acid residue or not present

<221> VARIANT

<222> (31)...(40)

<223> Each Xaa is independently any amino acid residue

<221> VARIANT

<222> (41)...(46)

<223> Each Xaa is independently any amino acid residue or not present

<221> VARIANT

<222> (48)...(48)

<223> Xaa is any amino acid residue

<400> 7

Xaa	Cys	Xaa	Xaa	Xaa	Xaa	Xaa	Cys	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa
1			5				10						15	
Xaa	Xaa	Cys	Xaa	Xaa	Cys	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Cys	Xaa	Xaa
			20				25						30	

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<213> Artificial Sequence

<223> Pseudo repeat motif #4

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<223> Each Xaa is independently any amino acid residue

<223> Each Xaa is independently any amino acid residue or not present

<223> Each Xaa is independently any amino acid residue

<223> Each Xaa is independently any amino acid residue

<223> Each Xaa is independently any amino acid residue

<223> Each Xaa is independently any amino acid residue or not present

<222> (35) ... (37)

<223> Each Xaa is independently any amino acid residue

<221> VARIANT

<222> (38)...(41)

<223> Each Xaa is independently any amino acid residue
or not present

<221> VARIANT

<222> (43)...(43)

<223> Each Xaa is independently any amino acid residue

<400> 8

Xaa	Cys	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa
1			5				10					15			
Cys	Xaa	Xaa	Cys	Xaa	Xaa	Cys	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa
			20				25					30			
Xaa	Cys	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Cys	Xaa					
			35				40								

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<211> 43

<212> PRT

<213> Artificial Sequence

<220>

<223> Pseudo repeat motif #4 alternative motif

<221> VARIANT

<222> (1)...(1)

<223> Xaa is any amino acid residue

<221> VARIANT

<222> (3)...(12)

<223> Each Xaa is independently any amino acid residue

<221> VARIANT

<222> (13)...(16)

<223> Each Xaa is independently any amino acid residue
or not present

<221> VARIANT

<222> (18)...(22)

<223> Each Xaa is independently any amino acid residue

<221> VARIANT
 <222> (24)...(27)
 <223> Each Xaa is independently any amino acid residue

<221> VARIANT
 <222> (28)...(33)
 <223> Each Xaa is independently any amino acid residue
 or not present

<221> VARIANT
 <222> (34)...(37)
 <223> Each Xaa is independently any amino acid residue

<221> VARIANT
 <222> (38)...(41)
 <223> Each Xaa is independently any amino acid residue
 or not present

<221> VARIANT
 <222> (43)...(43)
 <223> Xaa is any amino acid residue

<400> 9
 Xaa Cys Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
 1 5 10 15
 Cys Xaa Xaa Xaa Xaa Xaa Cys Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
 20 25 30
 Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Cys Xaa
 35 40

<210> 10
 <211> 18
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> oligonucleotide primer ZC25352

<400> 10
 ccttgcccag ttgttctc

<210> 11

<211> 18
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> oligonucleotide primer ZC25353

<400> 11
 tctggtggga tgggatag 18

<210> 12
 <211> 26
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> oligonucleotide primer ZC25364

<400> 12
 acctgtgctg tcatcaatcg tgttca 26

<210> 13
 <211> 24
 <212> DNA
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<220>
 <223> oligonucleotide primer ZC25365

<400> 13
 cccccaaggt ctcagctcca gtat 24

<210> 14
 <211> 18
 <212> DNA
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<220>
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<400> 14
 ccttgcccag ttgttctc 18

<210> 15
 <211> 18
 <212> DNA
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<220>
 <223> oligonucleotide primer ZC25353

<400> 15
 tctggtggga tgggatag

18

<210> 16
 <211> 6
 <212> PRT
 <213> Artificial protein

<400> 16
 Glu Tyr Met Pro Met Glu
 1 5

<210> 17
 <211> 33
 <212> DNA
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<220>
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<400> 17
 gcggatccga ttgccaagaa aatgagtact ggg

33

<210> 18
 <211> 37
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> oligonucleotide primer ZC25596

<400> 18
 gcagatctgg gctccactgt gggatcatct gcctcca

37

<210> 19
 <211> 108
 <212> DNA
 <213> Homo sapiens

<220>
 <223> tPA leader

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 tcgctcagcc aggaaatcca tgccgagttg agacgcttcc gtagatcc 108

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<220>
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 ccgtcagtct tcctcttccc cccaaaaccc aaggacaccc tcatgatctc ccggaccct 120
 gaggtcacat gcgtggtggt ggacgtgagc cacgaagacc ctgaggtcaa gttcaactgg 180
 tacgtggacg gcgtggaggt gcataatgcc aagacaaagc cgcgggagga gcagtacaac 240
 agcacgtacc gtgtggtcag cgtcctcacc gtcctgcacc aggactggct gaatggcaag 300
 gagtacaagt gcaagggtctc caacaaagcc ctcccatacct ccatcgagaa aaccatctcc 360
 aaagccaaaag ggcagccccg agaaccacag gtgtacaccc tgccccatc ccgggatgag 420
 ctgaccaaga accaggtcag cctgacctgc ctggtcaaag gttctatcc cagcgacatc 480
 gccgtggagt gggagagcaa tgggcagccg gagaacaact acaagaccac gcctcccgtg 540
 ctggactccg acggtcctt cttcctctac agcaagctca ccgtggacaa gagcaggtgg 600
 cagcagggga acgtcttctc atgctccgtg atgcatgagg ctctgcacaa ccactacacg 660
 cagaagagcc tctccctgtc tccgggtaaa taa 693

<210> 21
 <211> 534
 <212> DNA
 <213> Artificial sequence

<400> 21
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 aatgagtact gggaccaatg gggacggtgt gtcacctgcc aacggtgtgg tcctggacag 180

gagctatcca	aggattgtgg	ttatggagag	ggtggagatg	cctactgcac	agcctgccct	240
cctcgcaggt	acaaaagcag	ctggggccac	cacaaatgtc	agagttgcat	cacctgtgct	300
gtcatcaatc	gtgttcagaa	ggtcaactgc	acagctacct	ctaattgctgt	ctgtggggac	360
tgtttgccca	ggttctaccg	aaagacacgc	attggaggcc	tgcaggacca	agagtgcac	420
ccgtgcacga	agcagacccc	cacctctgag	gttcaatgtg	ccttcagtt	gagcttagtg	480
gaggcagatg	cacccacagt	ggagcccaga	tctgaatata	tgcccatgga	ataa	534

<210> 22

<211> 1200

<212> DNA

<213> Artificial Sequence

<220>

<223> construct

<400> 22

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aatgagtact	gggaccaatg	gggacggtgt	gtcacctgcc	aacgggtgtg	tcctggacag	180
gagctatcca	aggattgtgg	ttatggagag	ggtggagatg	cctactgcac	agcctgccct	240
cctcgcaggt	acaaaagcag	ctggggccac	cacaaatgtc	agagttgcat	cacctgtgct	300
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tgtttgccca	ggttctaccg	aaagacacgc	attggaggcc	tgcaggacca	agagtgcac	420
ccgtgcacga	agcagacccc	cacctctgag	gttcaatgtg	ccttcagtt	gagcttagtg	480
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tgcccagcac	ctgaagccga	gggggcaccg	tcagtcttcc	tcttcccccc	aaaacccaag	600
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ctgcaccagg	actggctgaa	tggcaaggag	tacaagtgca	aggtctccaa	caaagccctc	840
ccatcctcca	tcgagaaaac	catctccaaa	gccaaagggc	agccccgaga	accacagggtg	900
tacaccctgc	ccccatcccc	ggatgagctg	accaagaacc	aggtcagcct	gacctgcctg	960
gtcaaaggct	tctatcccag	cgacatcgcc	gtggagtggg	agagcaatgg	gcagccggag	1020
aacaactaca	agaccacgcc	tcccgtgctg	gactccgacg	gtccttctt	cctctacagc	1080
aagctcaccg	tggacaagag	caggtggcag	caggggaacg	tcttctcatg	ctccgtgatg	1140
catgaggctc	tgacaacca	ctacacgcag	aagagcctct	ccctgtctcc	gggtaataaa	1200

<210> 23

<211> 47

<212> DNA

<213> Artificial Sequence

<220>

<223> Oligonucleotide ZC26463

<400> 23

atgcattaac cctcactaaa ggccttcct ggggctcttc ttctct

47

<210> 24

<211> 46

<212> DNA

<213> Artificial Sequence

<220>

<223> Oligonucleotide ZC26464

<400> 24

taatacgact cactataggg aggggccct gctgctgttg tggtat

46

<210> 25

<211> 49

<212> DNA

<213> Artificial Sequence

<220>

<223> Oligonucleotide ZC26470

<400> 25

atgcattaac cctcactaaa gggacctgtg ctgtcatcaa tcgtgttca

49

<210> 26

<211> 47

<212> DNA

<213> Artificial Sequence

<220>

<223> Oligonucleotide ZC26471

<400> 26

taatacgact cactataggg agggcccca ggtctcagct ccagtat

47

<210> 27

<211> 297

<212> PRT

<213> Homo sapiens

<400> 27

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Tyr	Gly	Glu	Gly	Gly	Asp	Ala	Tyr	Cys	Thr	Ala	Cys	Pro	Pro	Arg	Arg	35	40	45	
Tyr	Lys	Ser	Ser	Trp	Gly	His	His	Lys	Cys	Gln	Ser	Cys	Ile	Thr	Cys	50	55	60	
Ala	Val	Ile	Asn	Arg	Val	Gln	Lys	Val	Asn	Cys	Thr	Ala	Thr	Ser	Asn	65	70	75	80
Ala	Val	Cys	Gly	Asp	Cys	Leu	Pro	Arg	Phe	Tyr	Arg	Lys	Thr	Arg	Ile	85	90	95	
Gly	Gly	Leu	Gln	Asp	Gln	Glu	Cys	Ile	Pro	Cys	Thr	Lys	Gln	Thr	Pro	100	105	110	
Thr	Ser	Glu	Val	Gln	Cys	Ala	Phe	Gln	Leu	Ser	Leu	Val	Glu	Ala	Asp	115	120	125	
Ala	Pro	Thr	Val	Pro	Pro	Gln	Glu	Ala	Thr	Leu	Val	Ala	Leu	Val	Ser	130	135	140	
Ser	Leu	Leu	Val	Val	Phe	Thr	Leu	Ala	Phe	Leu	Gly	Leu	Phe	Phe	Leu	145	150	155	160
Tyr	Cys	Lys	Gln	Phe	Phe	Asn	Arg	His	Cys	Gln	Arg	Gly	Gly	Leu	Leu	165	170	175	
Gln	Phe	Glu	Ala	Asp	Lys	Thr	Ala	Lys	Glu	Glu	Ser	Leu	Phe	Pro	Val	180	185	190	
Pro	Pro	Ser	Lys	Glu	Thr	Ser	Ala	Glu	Ser	Gln	Val	Ser	Glu	Asn	Ile	195	200	205	
Phe	Gln	Thr	Gln	Pro	Leu	Asn	Pro	Ile	Leu	Glu	Asp	Asp	Cys	Ser	Ser	210	215	220	
Thr	Ser	Gly	Phe	Pro	Thr	Gln	Glu	Ser	Phe	Thr	Met	Ala	Ser	Cys	Thr	225	230	235	240
Ser	Glu	Ser	His	Ser	His	Trp	Val	His	Ser	Pro	Ile	Glu	Cys	Thr	Glu	245	250	255	
Leu	Asp	Leu	Gln	Lys	Phe	Ser	Ser	Ser	Ala	Ser	Tyr	Thr	Gly	Ala	Glu	260	265	270	
Thr	Leu	Gly	Gly	Asn	Thr	Val	Glu	Ser	Thr	Gly	Asp	Arg	Leu	Glu	Leu	275	280	285	
Asn	Val	Pro	Phe	Glu	Val	Pro	Ser	Pro								290	295		

<210> 28
 <211> 891
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> degenerate sequence

<221> misc_feature
 <222> (1)...(891)
 <223> n = A,T,C or G

<400> 28

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atggaytgyc argaraayga rtaytgggag cartgggggnt gntgygtnac ntgyccarmgn      60
tgyggngccng gncargaryt nwsnaargay tgyggntayg gngarggngg ngaygcntay      120
tgyacngcnt gyccnccnmg nmgtayaar wsnwsntggg gncaycayaa rtgyccarwsn      180
tgyathacnt gygcngtnat haaymgngtn caraargtna aytgyacngc nacnwsnaay      240
gcngtntgyg gngaytgyyt nccnmgntty taymgnaara cnmgngathgg nggnytnear      300
gaycargart gyathccntg yacnaarcar acnccnacnw sngargtnca rtgygcntty      360
carytnwsny tngtngargc ngaygcncn acngtncnc cncargargc nacnytngt      420
gcnytngtnw snwsnytnyt ngtngtntty acnytnngnt tyytnggnyt nttyttyytn      480
taytgyaarc arttytyaa ymgncaytg carmgngng gnytnytnca rtytgargcn      540
gayaaracng cnaargarga rwsnytnntty ccngtncnc cnwsnaarga racnwsngcn      600
garwsncarg tnwsngaraa yathttycar acncarcny tnaayccnat hytnargay      660
gaytgywsnw snacnwsngg nttyccnacc cngarwsnt tyacnatggc nwsntgyacn      720
wsngarwsnc aywsncaytg ggtncaywsn ccnathgart gyacngaryt ngayytncar      780
aarttywsnw snwsngcnws ntayacnggn gcngaracny tngngngnaa yacngtngar      840
wsnacnggng aymgnytna rytnaaygtn ccnttygarg tnccnwsncc n      891
  
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<210> 29
 <211> 267
 <212> PRT
 <213> Homo sapiens

<400> 29

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Met Asp Cys Gln Glu Asn Glu Tyr Trp Asp Gln Trp Gly Arg Cys Val
 1             5             10             15
Thr Cys Gln Arg Cys Gly Pro Gly Gln Glu Leu Ser Lys Asp Cys Gly
      20             25             30
Tyr Gly Glu Gly Gly Asp Ala Tyr Cys Thr Ala Cys Pro Pro Arg Arg
      35             40             45
Tyr Lys Ser Ser Trp Gly His His Lys Cys Gln Ser Cys Ile Thr Cys
 50             55             60
  
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Ala Val Ile Asn Arg Val Gln Lys Val Asn Cys Thr Ala Thr Ser Asn
 65 70 75 80
 Ala Val Cys Gly Asp Cys Leu Pro Arg Phe Tyr Arg Lys Thr Arg Ile
 85 90 95
 Gly Gly Leu Gln Asp Gln Glu Cys Ile Pro Cys Thr Lys Gln Thr Pro
 100 105 110
 Thr Ser Glu Val Gln Cys Ala Phe Gln Leu Ser Leu Val Glu Ala Asp
 115 120 125
 Ala Pro Thr Val Pro Pro Gln Glu Ala Thr Leu Val Ala Leu Gly Gly
 130 135 140
 Leu Leu Gln Phe Glu Ala Asp Lys Thr Ala Lys Glu Glu Ser Leu Phe
 145 150 155 160
 Pro Val Pro Pro Ser Lys Glu Thr Ser Ala Glu Ser Gln Val Ser Glu
 165 170 175
 Asn Ile Phe Gln Thr Gln Pro Leu Asn Pro Ile Leu Glu Asp Asp Cys
 180 185 190
 Ser Ser Thr Ser Gly Phe Pro Thr Gln Glu Ser Phe Thr Met Ala Ser
 195 200 205
 Cys Thr Ser Glu Ser His Ser His Trp Val His Ser Pro Ile Glu Cys
 210 215 220
 Thr Glu Leu Asp Leu Gln Lys Phe Ser Ser Ser Ala Ser Tyr Thr Gly
 225 230 235 240
 Ala Glu Thr Leu Gly Gly Asn Thr Val Glu Ser Thr Gly Asp Arg Leu
 245 250 255
 Glu Leu Asn Val Pro Phe Glu Val Pro Ser Pro
 260 265

<210> 30
 <211> 801
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> degenerate sequence

<221> misc_feature
 <222> (1)...(801)
 <223> n = A,T,C or G

<400> 30

atggaytgyc	argaraayga	rtaytggg	cartggggnm	gntgygtnac	ntgycarmgn	60
tgyggncng	gncargaryt	nwsnaargay	tgyggntayg	gngargngg	ngaygcntay	120
tgyacngcnt	gyccnccnmg	nmgntayaar	wsnwsntggg	gncaycayaa	rtgycarwsn	180

tgyathacnt	gygcngtnat	haaymgngtn	caraargtna	aytgyacngc	nacnwsnaay	240
gcngtntgyg	gngaytgyyt	nccnmgnTTY	taymgnaara	cnmgcnathgg	nggnytnear	300
gaycargart	gyathccntg	yacnaarcar	acnccnacnw	sngargtnca	rtgygcntty	360
carytnwsny	tngtngargc	ngaygcncn	acngtncnc	cncargargc	nacnytngt	420
gcnytnggng	gnytnytnc	rttygargcn	gayaaracng	cnaargarga	rwsnytnntty	480
ccngtncnc	cnwsnaarga	racnwsngcn	garwsncarg	tnwsngaraa	yathttycar	540
acncarccny	tnaayccnat	hytngargay	gaytgywsnw	snacnwsngg	nttyccnacn	600
cargarwsnt	tyacnatggc	nwsntgyacn	wsngarwsnc	aywsncaytg	ggtncayswn	660
ccnathgart	gyacngaryt	ngayytncar	aarttywsnw	snwsngcnws	ntayacnggn	720
gcngaracny	tngnggnaa	yacngtngar	wsnacngng	aymgnytna	rytnaaygt	780
ccnttygarg	tnccnwsncc	n				801

<210> 31

<211> 529

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> (1)...(529)

<223> n = A,T,C or G

<400> 31

ggattcnatn	nctgaggntg	natggcnttc	nagttnwgas	tkagtggagg	cagatgcasc	60
cacagtcccc	gcctcaggag	gycacacttg	ttgcrmtggt	gagcagcstg	ctagtgggtgt	120
ttrccctggc	cttccctggg	ctcttcttcc	tcwacygcaa	gcagttcttc	aacagacatt	180
gycagcsgng	gaggtttgct	gcagtttgag	gctgatraaa	cagcaaagga	ggaatctstm	240
ttycycgtgc	cacccagcaa	ggagaccagt	gctgagtccc	aagtgagtga	gaacatyttt	300
cakacccagm	cacttaaccc	tatcctyrac	gacgactgca	rtcgactag	tggyttcccc	360
acacaggart	metttaccat	ggcctyctgc	acctyagaga	gccactacca	ctgggwccac	420
arccccatcg	aatgcacaka	gctggacctg	caaaagtttt	ccagctctgc	ctcctatact	480
ggagctgara	ccttgggggg	aaacacagnc	aaaagcactg	ganacaggg		529

<210> 32

<211> 401

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> (1)...(401)

<223> n = A,T,C or G

<400> 32

cagttgagct tagtgaggc agatgcaccc acagtgcacc ctcaggaggc cacacttggt	60
gsactggagg ttgtctgcag tttagaggctg ataaaacagc aaaggaggaa tctctcttts	120
ccgtgccacc cagcaaggag accagtgcgt agtcccaagt gactgagaac atctttcaga	180
cccagccact taaccctatc ctcaggagc actgcagctc gactagtggc tccccacac	240
aggagtcctt taccatggcc tctgcacct .cagagagcca ctcccactgg gtccacagcc	300
ccatcgaatg cacagagctg gacctgcaa agttttccag ctctgcctcc tatactggag	360
ctgagacctt ggggggaaac acagtcgaaa gcactggaga c	401

<210> 33

<211> 528

<212> DNA

<213> Homo sapiens

<400> 33

ctctgagggt caatgtgcct tccagttgag cttagtggag gcagatgcac ccacagtgcc	60
ccctcaggag gccacacttg ttgcactggt gacagcctg ctagtgggtt ttaccctggc	120
cttctctggg ctcttcttcc tctactgcaa gcagttcttc aacagacatt gccagcgtgt	180
tgcaggaggt ttgtctgcag ttgaggctga taaaacagca aaggagggaat ctctcttccc	240
cgtgccaccc agcaaggaga ccagtgcgtg gtcccaagtg agtgagaaca tctttcagac	300
ccagccactt aaccctatcc tcgaggacga ctgcagctcg actagtggct tccccacaca	360
ggagtccttt accatggcct cctgcacctc agagagccac tcccactggg tccacagccc	420
catcgaatgc acagagctgg acctgcaaaa gttttccagc tctgcctcct atactggagc	480
tgagaccttg gggggaaaca cagtcgaaag cactggagac aggctgga	528

<210> 34

<211> 175

<212> PRT

<213> Homo sapiens

<400> 34

Ser Glu Val Gln Cys Ala Phe Gln Leu Ser Leu Val Glu Ala Asp Ala	
1 5 10 15	
Pro Thr Val Pro Pro Gln Glu Ala Thr Leu Val Ala Leu Val Ser Ser	
20 25 30	
Leu Leu Val Val Phe Thr Leu Ala Phe Leu Gly Leu Phe Phe Leu Tyr	
35 40 45	
Cys Lys Gln Phe Phe Asn Arg His Cys Gln Arg Val Ala Gly Gly Leu	
50 55 60	
Leu Gln Phe Glu Ala Asp Lys Thr Ala Lys Glu Glu Ser Leu Phe Pro	
65 70 75 80	
Val Pro Pro Ser Lys Glu Thr Ser Ala Glu Ser Gln Val Ser Glu Asn	
85 90 95	

Ile Phe Gln Thr Gln Pro Leu Asn Pro Ile Leu Glu Asp Asp Cys Ser
 100 105 110
 Ser Thr Ser Gly Phe Pro Thr Gln Glu Ser Phe Thr Met Ala Ser Cys
 115 120 125
 Thr Ser Glu Ser His Ser His Trp Val His Ser Pro Ile Glu Cys Thr
 130 135 140
 Glu Leu Asp Leu Gln Lys Phe Ser Ser Ser Ala Ser Tyr Thr Gly Ala
 145 150 155 160
 Glu Thr Leu Gly Gly Asn Thr Val Glu Ser Thr Gly Asp Arg Leu
 165 170 175

<210> 35
 <211> 299
 <212> PRT
 <213> Homo sapiens

<400> 35
 Met Asp Cys Gln Glu Asn Glu Tyr Trp Asp Gln Trp Gly Arg Cys Val
 1 5 10 15
 Thr Cys Gln Arg Cys Gly Pro Gly Gln Glu Leu Ser Lys Asp Cys Gly
 20 25 30
 Tyr Gly Glu Gly Gly Asp Ala Tyr Cys Thr Ala Cys Pro Pro Arg Arg
 35 40 45
 Tyr Lys Ser Ser Trp Gly His His Lys Cys Gln Ser Cys Ile Thr Cys
 50 55 60
 Ala Val Ile Asn Arg Val Gln Lys Val Asn Cys Thr Ala Thr Ser Asn
 65 70 75 80
 Ala Val Cys Gly Asp Cys Leu Pro Arg Phe Tyr Arg Lys Thr Arg Ile
 85 90 95
 Gly Gly Leu Gln Asp Gln Glu Cys Ile Pro Cys Thr Lys Gln Thr Pro
 100 105 110
 Thr Ser Glu Val Gln Cys Ala Phe Gln Leu Ser Leu Val Glu Ala Asp
 115 120 125
 Ala Pro Thr Val Pro Pro Gln Glu Ala Thr Leu Val Ala Leu Val Ser
 130 135 140
 Ser Leu Leu Val Val Phe Thr Leu Ala Phe Leu Gly Leu Phe Phe Leu
 145 150 155 160
 Tyr Cys Lys Gln Phe Asn Arg His Cys Gln Arg Val Ala Gly Gly
 165 170 175
 Leu Leu Gln Phe Glu Ala Asp Lys Thr Ala Lys Glu Glu Ser Leu Phe
 180 185 190
 Pro Val Pro Pro Ser Lys Glu Thr Ser Ala Glu Ser Gln Val Ser Glu
 195 200 205

Asn Ile Phe Gln Thr Gln Pro Leu Asn Pro Ile Leu Glu Asp Asp Cys
 210 215 220
 Ser Ser Thr Ser Gly Phe Pro Thr Gln Glu Ser Phe Thr Met Ala Ser
 225 230 235 240
 Cys Thr Ser Glu Ser His Ser His Trp Val His Ser Pro Ile Glu Cys
 245 250 255
 Thr Glu Leu Asp Leu Gln Lys Phe Ser Ser Ser Ala Ser Tyr Thr Gly
 260 265 270
 Ala Glu Thr Leu Gly Gly Asn Thr Val Glu Ser Thr Gly Asp Arg Leu
 275 280 285
 Glu Leu Asn Val Pro Phe Glu Val Pro Ser Pro
 290 295

<210> 36
 <211> 431
 <212> DNA
 <213> Homo sapiens

<400> 36
 ctc tga ggt tca atg tgc ctt cca gtt gag ctt agt gga ggc aga tgc 48
 acc cac agt gcc ccc tca gga ggc cac act tgt tgc act gga ggt ttg 96
 ctg cag ttt gag gct gat aaa aca gca aag gag gaa tct ctc ttc ccc 144
 gtg cca ccc agc aag gag acc agt gct gag tcc caa gtg agt gag aac 192
 atc ttt cag acc cag cca ctt aac cct atc ctc gag gac gac tgc agc 240
 tcg act agt ggc ttc ccc aca cag gag tcc ttt acc atg gcc tcc tgc 288
 acc tca gag agc cac tcc cac tgg gtc cac agc ccc atc gaa tgc aca 336
 gag ctg gac ctg caa aag ttt tcc agc tct gcc tcc tat act gga gct 384
 gag acc ttg ggg gga aac aca gtc gaa agc act gga gac agg ctg ga 431

<210> 37
 <211> 142
 <212> PRT
 <213> Homo sapiens

<400> 37
 Leu Gly Ser Met Cys Leu Pro Val Glu Leu Ser Gly Gly Arg Cys Thr
 1 5 10 15
 His Ser Ala Pro Ser Gly Gly His Thr Cys Cys Thr Gly Gly Leu Leu
 20 25 30
 Gln Phe Glu Ala Asp Lys Thr Ala Lys Glu Glu Ser Leu Phe Pro Val
 35 40 45
 Pro Pro Ser Lys Glu Thr Ser Ala Glu Ser Gln Val Ser Glu Asn Ile
 50 55 60

Phe	Gln	Thr	Gln	Pro	Leu	Asn	Pro	Ile	Leu	Glu	Asp	Asp	Cys	Ser	Ser
65					70				75					80	
Thr	Ser	Gly	Phe	Pro	Thr	Gln	Glu	Ser	Phe	Thr	Met	Ala	Ser	Cys	Thr
				85					90					95	
Ser	Glu	Ser	His	Ser	His	Trp	Val	His	Ser	Pro	Ile	Glu	Cys	Thr	Glu
			100					105					110		
Leu	Asp	Leu	Gln	Lys	Phe	Ser	Ser	Ser	Ala	Ser	Tyr	Thr	Gly	Ala	Glu
		115					120					125			
Thr	Leu	Gly	Gly	Asn	Thr	Val	Glu	Ser	Thr	Gly	Asp	Arg	Leu		
	130					135					140				

<210> 38

<211> 173

<212> PRT

<213> Homo sapiens

<400> 38

Met	Asp	Cys	Gln	Glu	Asn	Glu	Tyr	Trp	Asp	Gln	Trp	Gly	Arg	Cys	Val
1				5					10				15		
Thr	Cys	Gln	Arg	Cys	Gly	Pro	Gly	Gln	Glu	Leu	Ser	Lys	Asp	Cys	Gly
			20					25					30		
Tyr	Gly	Glu	Gly	Gly	Asp	Ala	Tyr	Cys	Thr	Ala	Cys	Pro	Pro	Arg	Arg
	35					40					45				
Tyr	Lys	Ser	Ser	Trp	Gly	His	His	Lys	Cys	Gln	Ser	Cys	Ile	Thr	Cys
	50					55					60				
Ala	Val	Ile	Asn	Arg	Val	Gln	Lys	Val	Asn	Cys	Thr	Ala	Thr	Ser	Asn
65					70					75				80	
Ala	Val	Cys	Gly	Asp	Cys	Leu	Pro	Arg	Phe	Tyr	Arg	Lys	Thr	Arg	Ile
			85						90					95	
Gly	Gly	Leu	Gln	Asp	Gln	Glu	Cys	Ile	Pro	Cys	Thr	Lys	Gln	Thr	Pro
		100						105					110		
Thr	Ser	Glu	Val	Gln	Cys	Ala	Phe	Gln	Leu	Ser	Leu	Val	Glu	Ala	Asp
	115					120						125			
Ala	Pro	Thr	Val	Pro	Pro	Gln	Glu	Ala	Thr	Leu	Val	Ala	Leu	Glu	Val
	130					135					140				
Cys	Cys	Ser	Leu	Arg	Leu	Ile	Lys	Gln	Gln	Arg	Arg	Asn	Leu	Ser	Ser
145					150					155				160	
Pro	Cys	His	Pro	Ala	Arg	Arg	Pro	Val	Leu	Ser	Pro	Lys			
				165						170					

<210> 39

<211> 519

<212> DNA

<213> Artificial Sequence

<220>

<223> degenerate polynucleotide sequence

<221> misc_feature

<222> (1)...(519)

<223> n = A,T,C or G

<400> 39

atggaytgyc argaraayga rtaytgggay cartggggnm gntgygtnac ntgycarmgn	60
tgyggncng gncargaryt nwsnaargay tgyggntayg gngarggngg ngaygcntay	120
tgyacngent gyccnccnmg nmgtayaar wsnwsntggg gncaycayaa rtgycarwsn	180
tgyathacnt gygcngtnat haaymgngtn caraargtna aytgyacngc nacnwsnaay	240
gcngtntgyg gngaytgyyt nccnmgntty taymgnaara cnmgnathgg nggnytnear	300
gaycargart gyathccntg yacnaarcar acnccnacnw sngargtnca rtgygcntty	360
carytnwsny tngtngargc ngaygcncn acngtnccnc cncargargc nacnytnngtn	420
gcnytnarg tntgytgyws nytnmgnytn athaarcarc armgmgnaa yytnwsnwsn	480
cctngycayc cngcnmgnmg nccngtnytn wsnccnaar	519

<210> 40

<211> 47

<212> DNA

<213> Artificial Sequence

<220>

<223> oligonucleotide ZC26463

<400> 40

atgcattaac cctcactaaa gggccttcct ggggctcttc ttcctct	47
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<210> 41

<211> 46

<212> DNA

<213> Artificial Sequence

<220>

<223> Oligonucleotide sequence ZC 26464

<400> 41

taatacgact cactataggg aggggccct gctgctgttg tggtat	46
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<210> 42

<211> 49
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Oligonucleotide ZC24670

<400> 42
 atgcattaac cctcactaaa gggacctgtg ctgtcatcaa tcgtgttca 49

<210> 43
 <211> 47
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Oligonucleotide sequence ZC 26471

<400> 43
 taatacgact cactataggg agggccccc aa ggtctcagct ccagtat 47

<210> 44
 <211> 657
 <212> DNA
 <213> murine

<400> 44
 ggtggcatct ctcttccaat tggctctgatt gttggagtga catcactggg tctgctgatg 60
 ttaggactgg tgaactgcat catcctgggt cagaggaaaa agaagccctc ctgcctacaa 120
 agagatgcca aggtgcctca tgtgcctgat gagaaatccc aggatgcagt aggccttgag 180
 cagcagcacc tgttgaccac agcaccaggt tccagcagca gctccctaga gagctcagcc 240
 agcgctgggg accgaagggc gcccctggg ggccatcccc aagcaagagt catggcggag 300
 gcccaagggt ttcaggaggc ccgtgccagc tccaggattt cagattcttc ccacggaagc 360
 cacgggaccc acgtcaacgt cacctgcacg gtgaacgtct gtagcagctc tgaccacagt 420
 tctcagtgtc cttcccaagc cagcgccaca gtgggagacc cagatgccaa gccctcagcg 480
 tccccaaagg atgagcaggt ccccttctct caggaggagt gtccgtctca gtccccgtgt 540
 gagactacag agacactgca gagccatgag aagcccttgc cccttggtgt gccgatatg 600
 ggcatgaagc ccagccaagc tggctggttt gatcagattg cagtcaaagt ggcctga 657

<210> 45
 <211> 824
 <212> DNA

<213> Artificial Sequence

<220>

<223> artificial cDNA sequence

<400> 45

ggtaccgaat tgtacgcgta tggggacttc ccatatcaat cagggacttt ccgctgggga	60
ctttccggtc tgactcatgc ttctgactca tgcttggtg acatcatctc gactagtcgt	120
accttcccgt aaatccctcc cttcccga attacacacg cgtatttccc agaaaaggaa	180
ctgtagattt ctaggaattc aatccttggc cagcggtta caccggaagt tttccatatt	240
aggaattcct tccggtttcc tttctcgagg ccacgtggt tgagcccgcac actcattcat	300
aaaacgcttg ttataaaagc agtggctgcg ggccttcgt actccaaccg catctgcagc	360
gagcaactga gaagccaagg atccaggctg aattcatggg tctcaacccc cagctagttg	420
tcacctgct cttctttctc gaatgtacca ggagccatat ccacggatgc gacaaaaatc	480
acttgagaga gatcatcggc attttgaacg aggtcacagg agaagggacg ccatgcacgg	540
agatggatgt gccaaacgtc ctcacagcaa cgaagaacac cacagagagt gagctcgtct	600
gtagggcttc caaggtgctt cgcataatatt atttaaaaca tgggaaaact ccatgcttga	660
agaagaactc tagtgttctc atggagctgc agagactctt tcgggctttt cgatgcctgg	720
attcatcgat aagctgcacc atgaatgagt ccaagtccac atcactgaaa gacttcctgg	780
aaagcctaaa gagcatcatg caaatggatt actcgtagtc taga	824

<210> 46

<211> 47

<212> DNA

<213> Artificial Sequence

<220>

<223> Oligonucleotide sequence ZC28835

<400> 46

taatacgact cactataggg agggccccc aa ggtctcagct ccagtat	47
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<210> 47

<211> 27

<212> DNA

<213> Artificial Sequence

<220>

<223> Oligonucleotide sequence ZC 28836

<400> 47

gcaccggtgg cctcctgagg gggcact

27

<210> 48
 <211> 29
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Oligonucleotide ZC 28830

<400> 48
 gcaccggtgg catctctctt ccaattggt

29

<210> 49
 <211> 29
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Oligonucleotide ZC 28837

<400> 49
 gctctagagg ggtaggcca ctttgactg

29

<210> 50
 <211> 1081
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> DNA construct

<400> 50
 atggattgcc aagaaaatga gtactgggac caatggggac ggtgtgtcac ctgccaacgg 60
 tgtggtcctg gacaggagct atccaaggat tgtggttatg gagagggtgg agatgcctac 120
 tgcacagcct gccctcctcg caggtaaaa agcagctggg gccaccacaa atgtcagagt 180
 tgcatacct gtgctgtcat caatcgtgtt cagaaggcca actgcacagc tacctctaat 240
 gctgtctgtg gggactgttt gccaggttc taccgaaaga cacgcattgg aggctgcag 300
 gaccaagagt gcatcccgtg cacgaagcag acccccacct ctgagggtca atgtgccttc 360
 cagttgagct tagtgaggc agatgcaccc acagtgcacc ctcaggaggt caccgttggc 420
 atctctcttc caattggtct gattgttgga gtgacatcac tgggtctgct gatgttagga 480
 ctggtgaact gcatcatcct ggtgcagagg aaaaagaagc cctcctgcct acaaagagat 540
 gccaaaggcg ctcattgtgc tgatgagaaa tcccaggatg cagtaggcct tgagcagcag 600

cacctgttga	ccacagcacc	cagttccagc	agcagctccc	tagagagctc	agccagcgct	660
ggggaccgaa	gggcgcccc	tgggggcat	ccccaagcaa	gagtcatggc	ggaggcccaa	720
gggtttcagg	aggcccgtgc	cagctccagg	atttcagatt	cttcccacgg	aagccacggg	780
acccacgtca	acgtcacctg	catcgtgaac	gtctgtagca	gctctgacca	cagttctcag	840
tgctcttccc	aagccagcgc	cacagtggga	gaccagatg	ccaagccctc	agcgtcccca	900
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a						1081